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OM Protein - protein search, using sw model

Run on: October 22, 2001, 01:26:59 ; Search time 33.83 Seconds

Perfect score: 1643

Sequence: 1 MAGGRGAPGGRDEPPESYP.....YNIKVEKKVSTLFLYSYRDD 1643

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_minc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodont:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score being printed, and is derived by analysis of the result distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1467	89.3	1495	4	Q9P2K8	Q9p2k8 homo sapien
2	932	56.7	938	4	Q9NSQ3	Q9nsg3 homo sapien
3	785	47.8	806	4	Q9i5K1	Q9i5k1 homo sapien
4	510	31.0	548	4	Q9UJ56	Q9uj56 homo sapien
5	185	11.3	191	4	Q9NS25	Q9nzs5 homo sapien
6	85	5.2	1648	11	Q9QZ05	Q9qz05 mus musculus
7	82	5.0	1370	11	Q9ESB8	Q9esb8 mus musculus
8	82	5.0	1570	11	Q9ESB6	Q9esb6 mus musculus
9	82	5.0	1648	11	Q9ESB7	Q9esb7 mus musculus
10	14	0.9	1589	5	Q9E551	Q9e551 drosophila
11	14	0.9	1589	5	Q91712	Q9i712 drosophila
12	14	0.9	1589	5	Q9V9X8	Q9v9x8 drosophila
13	11	0.7	576	5	Q9WVB2	Q9wvb2 drosophila
14	10	0.6	285	13	Q9DEB2	Q9deb2 seriola qui
15	10	0.6	301	6	Q9055	Q9055 papiro hamad
16	10	0.6	307	13	Q90458	Q90458 brachydanio
17	10	0.6	312	5	Q17349	Q17349 caenorhabdi
18	10	0.6	359	14	Q85153	Q85153 murine sarc
19	10	0.6	375	14	Q67624	Q67624 ic4 retrov

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score being printed, and is derived by analysis of the result distribution.

ALIGNMENTS

Result	No.	Score	Query	Match	Length	DB ID	Description
1	20	10	10	0.6	420	13	Q90893 gallus gallus
	21	22	10	0.6	421	4	Q15278 homo sapien
	22	23	10	0.6	462	10	Q39886 glycine max
	23	24	10	0.6	506	14	Q85632 avian retro
	24	25	10	0.6	598	13	P70032 xenopus lae
	25	26	10	0.6	602	11	Q63485 ratius norv
	26	27	10	0.6	615	5	Q20845 canenorhabdi
	27	28	10	0.6	632	5	Q9UA36 canenorhabdi
	28	29	10	0.6	632	5	Q9N2L7 canenorhabdi
	29	30	10	0.6	636	5	Q9Y1J3 canenorhabdi
	30	31	10	0.6	649	5	Q76763 canenorhabdi
	31	32	10	0.6	651	4	Q9Y6T3 canenorhabdi
	32	33	10	0.6	739	5	Q9W4Z3 drosophila
	33	34	10	0.6	782	5	Q9NEH9 drosophila
	34	35	10	0.6	813	5	Q9NA4E3 c. elegan
	35	36	10	0.6	903	3	Q9HGN1 schizosacch
	36	37	10	0.6	1106	13	Q42291 gallus gallus
	37	38	10	0.6	1646	3	Q74297 neurospora
	38	39	10	0.6	1696	5	Q9XVY4 canenorhabdi
	39	40	9	0.5	557	13	Q91566 xenopus lae
	40	41	9	0.5	62	5	Q9TwZ7 lycechinus
	41	42	9	0.5	68	13	Q90961 gallus gallus
	42	43	9	0.5	133	5	Q9X121 ephydiasia
	43	44	9	0.5	219	5	Q9Y1Y9 ephydiasia
	44	45	9	0.5	226	10	Q9FFP0 arabiopsis

Query Match 89.3%; Score 1457; DB 4; Length 1495; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1
ID Q9P2K8 PRELIMINARY; PRT; 1495 AA.
ID Q9p2k8 AC
ID Q92K8 DT 01-OCT-2000 (TREMBLrel. 15, Created)
ID Q92K8 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
ID Q92K8 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KIAA1338 PROTEIN (FRAGMENT).
GN KIAA1338.
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TaxID=9606; RN [1]_SEQUENCE FROM N.A.
RX TISSUE-BRAIN; RC MEDLINE=20181126; PubMed=10718198; RA Nagase T; Kikuno R.; Ishikawa K.; Hiroawa M.; Ohara O.; RT "Prediction of the coding sequences of unidentified human genes XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro."; RL DNA Res. 7:65-73 (2000).
RT "SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES."; DR InterPro; IPR00719; -. CC AB037755; BAA92576.1; -. DR InterPro; IPR002280; -. DR Pfam; PF00069; kinase; 4. DR PROSITE; PS00116; DNA-POLYMERASE_B; UNKNOWN_1. DR PROSITE; PS00107; PROTEIN KINASE_AP; 1. DR PROSITE; PS50011; PROTEIN KINASE_DM; 2. DR SMART; SM00220; S_TKc; 1. KW ATP-binding; Serine/threonine-protein kinase; Transferase. FT NON_TER 1 1 SEQUENCE 1495 AA; 169334 MW; C7273209FE038D9 CRC64;

Db	1103	LYFKTEQKGDQLDMLPTNSLIKQTKTGTQALVKYKGKDLBEVGLKKGKIKLQVLNLG	1162
Db	1137	LYVKYQHQHNGLIFOFVAFIKRQRQAVPELLAAGGRDYLIPQFRGPOALGPVTAIGVSI	1376
Qy	1163	LYVKYQHQHNGLIFOFVAFIKRQRQAVPELLAAGGRDYLIPQFRGPOALGPVTAIGVSI	1222
Db	1223	AIDKISAAVINMEESVTISCDLIVSVQGMSMRAINTLQKLWAGTATEIMYDWSQSQ	1282
Qy	1377	AIDKISAAVINMEESVTISCDLIVSVQGMSMRAINTLQKLWAGTATEIMYDWSQSQ	1436
Db	1283	EELQEYCRHBIETTYALVSDKEGSHVKYKSFERQTEKRVLETELVDHVQLKFTKVTD	1342
Qy	1437	EELQEYCRHBIETTYALVSDKEGSHVKYKSFERQTEKRVLETELVDHVQLKFTKVTD	1496
Db	1283	EELQEYCRHBIETTYALVSDKEGSHVKYKSFERQTEKRVLETELVDHVQLKFTKVTD	1402
Qy	1497	ERNGREASDNIAVNQKGSFSNAGLSEFHGATVVPISVLAPEKLSASTRRYETQVQT	1556
Db	1343	ERNGREASDNIAVNQKGSFSNAGLSEFHGATVVPISVLAPEKLSASTRRYETQVQT	1402
Qy	1557	RQGTSNLANHQSEIEILAVDLPKETILQFLSLEDADEQAFNTTVYQQLSLRPLPKQRYL	1616
Db	1403	RQGTSNLANHQSEIEILAVDLPKETILQFLSLEDADEQAFNTTVYQQLSLRPLPKQRYL	1467
Qy	1617	KYVCDTEYNKVEKKVSVLFYLYSYRDD	1643
Qy	1463	KYVCDTEYNKVEKKVSVLFYLYSYRDD	1489
Db			
RESULT 2			
Q9NSQ3	2	PRELIMINARY; PRT; 938 AA.	
ID	Q9NSQ3		
AC	Q9NSQ3;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DR	HYPOTHETICAL 106.8 KDA PROTEIN (FRAGMENT).		
DE	DKEFPZ34F1312.		
GN	homo sapiens (Human).		
OS	Hominoidea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-TESTIS;		
RA	Duesterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S. ;		
RA	Submitted (Feb '2000) to the EMBL/GenBank/DBJ databases.		
RC	-!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.		
DR	EMBL: AL1157497; CAB75678.1; -.		
DR	InterPro: IPR000719; -.		
DR	InterPro: IPR00290; -.		
DR	Pfam: PF00069; kinase_1.		
DR	PROSITE: PS50011; PROTEIN_KINASE_DOMAIN.		
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.		
DR	SMART: SM00220; S_TK_C; 1.		
DR	ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;		
KW	ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;		
KW	transf erase.		
FT	NON_TER 1 MW: 98623F61FB44306D CRC64;		
SEQUENCE	938 AA; 106807 MW;		
SQ			
Query Match	56.7%	Score 932; DB 4; Length 938;	
Best Local Similarity	100.0%	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0	
Matches	932; Conservative		
Qy	712	STSGERSASARFPATGPQSSDDEDDDEBHGCVFSQSFPLASDSESDDIDFNEDNSKQ	77
Db	1	STSGERSASARFPATGPQSSDDEDDDEBHGCVFSQSFPLASDSESDDIDFNEDNSKQ	66
Qy	772	MQEDCNEKNGCHESSEPSVTTEAVHLYTQMEYCEKSLRDTDQGLYRTVRLWLFRE	8
Db	61	MQEDCNEKNGCHESSEPSVTTEAVHLYTQMEYCEKSLRDTDQGLYRTVRLWLFRE	1
Qy	832	ILDGLAYTHEKGMIHRDLKPVNIFLDSDDHVKIGDFGLATDIFASADSKODQTGDLIK	8

Db	121	ILDGLAYIHEGMIRHDLKPVNIFLDDDHVKIGDEGLATDHLAFSADSQDDOTGDLIK	180	RT "NEDO human cDNA sequencing project.";
QY	892	SOPSGHLTGMVGTALLYSPVEQGTSKSYAQKVDFSLGTLTTEFMSYHDMVTASERIYV	951	DR Submitted (Aug-2001: BAB15621; 1);
Db	181	SOPSGHLTGMVGTALLYSPVEQGTSKSYAQKVDFSLGTLTTEFMSYHDMVTASERIYV	240	DR EMBL: Ak027011; BAB15621; 1;
QY	952	NQLRDPTSPKPEPFDGEGHAKQKSYISWLINHDPAKRPTATELLKSELLPPOMEESEL	1011	SQ SEQUENCE 806 AA; 92006 MN; C5DBC4D2A990C4E43 CRC64;
Db	241	NQLRDPTSPKPEPFDGEGHAKQKSYISWLINHDPAKRPTATELLKSELLPPOMEESEL	300	Query Match 47.8%; Score 785; DB 4; Length 806;
QY	1012	HEVLHHTLTNVDGKAYRTMMQAQFQRSPIDTYDSDILKGNSFIRTAKMQOHVCETI	1071	Best Local Similarity 100.0%; Pred. No. 0;
Db	301	HEVLHHTLTNVDGKAYRTMMQAQFQRSPIDTYDSDILKGNSFIRTAKMQOHVCETI	360	Matches 785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1072	TRIEKRGAVOLCPTPLPDRQIYEHNEALEDHSGMLVMLPDLRIPFARYVARNNI	1131	QY 859 DDHVKGIGDGLATDHLASADSQDDOTGDLIKSDPSGHLTGMVGTALLYSPVEQGTSK 918
Db	361	TRIEKRGAVOLCPTPLPDRQIYEHNEALEDHSGMLVMLPDLRIPFARYVARNNI	420	Db 16 DDHVKGIGDGLATDHLASADSQDDOTGDLIKSDPSGHLTGMVGTALLYSPVEQGTSK 75
QY	1132	LNLRKRCIERNFRPKLDRFHPKELCADIIVSTTNSPLPTAEIYTTEIQEFPAL	1191	QY 919 AYNOKVDFLSGLTTEFMSYHPMVTASERIFVNLQDPTSPKPEPFDGEGHAKQKSY 978
Db	421	LNLRKRCIERNFRPKLDRFHPKELCADIIVSTTNSPLPTAEIYTTEIQEFPAL	480	Db 76 AYNOKVDFLSGLTTEFMSYHPMVTASERIFVNLQDPTSPKPEPFDGEGHAKQKSY 135
QY	1192	QERNYSTYLNTMLLKAILLHGCGIPEDKLQSQVITYLDAVEKLTTRREVEAKFCNLSS	1251	QY 979 SWLNHDAKRPATATELLKSELLPPOMEESELHEVLIHETLNVGKAYRTMMQAQFQSQR 1038
Db	481	QERNYSTYLNTMLLKAILLHGCGIPEDKLQSQVITYLDAVEKLTTRREVEAKFCNLSS	540	Db 136 SWLNHDAKRPATATELLKSELLPPOMEESELHEVLIHETLNVGKAYRTMMQAQFQSQR 195
QY	1252	NSLCRLYKFTIERSQKGDIDQLMFTINSLIKQKGTIAQLVKGKQDLEEVVGLKKIGLKQV	1311	QY 1039 ISPAIDTYDSDILKGNSFIRTAKMQOHVCETIIRIRKRGAVQLCPLPRLPNRQTEH 1098
Db	541	NSLCRLYKFTIERSQKGDIDQLMFTINSLIKQKGTIAQLVKGKQDLEEVVGLKKIGLKQV	600	Db 196 ISPAIDTYDSDILKGNSFIRTAKMQOHVCETIIRIRKRGAVQLCPLPRLPNRQTEH 255
QY	1312	LINLGLYKQIOHNGLIFQFVAFIKRRQRAVEPEILLAAGGRYDLIIPQFRGPQALGPVPTA	1371	QY 1099 NEAALFMDHSGMLVMLPDLRIPFARYVARNNIILKRYCILERVFRPKLDRFHPKELLE 1158
Db	601	LINLGLYKQIOHNGLIFQFVAFIKRRQRAVEPEILLAAGGRYDLIIPQFRGPQALGPVPTA	660	Db 256 NEAALFMDHSGMLVMLPDLRIPFARYVARNNIILKRYCILERVFRPKLDRFHPKELLE 315
QY	1372	IGVSIATDKISAAVLMNEESTVITSSCDLIVWSVGOMSMSRAINLTKLWTAGTAAIMYD	1431	QY 1159 CAFDIVTTNSNLEPTABILTYEIQEFPALQERNYSIYLNHTMLKATLHCGIPED 1218
Db	661	IGVSIATDKISAAVLMNEESTVITSSCDLIVWSVGOMSMSRAINLTKLWTAGTAAIMYD	720	Db 316 CAFDIVTTNSNLEPTABILTYEIQEFPALQERNYSIYLNHTMLKATLHCGIPED 375
QY	1432	WSQSQBLQEQCRHETITYVALVSKEGSHVKSFEKERQTERVLEFLDVHVLQKLR	1491	QY 1219 KLSQVYILLYDAVEKLTTRREVEAKFCNLSSNSLQRCPYKIEQKGDQLDMLPTINSLI 1278
Db	721	WSQSQBLQEQCRHETITYVALVSKEGSHVKSFEKERQTERVLEFLDVHVLQKLR	780	Db 376 KLSQVYILLYDAVEKLTTRREVEAKFCNLSSNSLQRCPYKIEQKGDQLDMLPTINSLI 435
QY	1492	TKVTDERNGRFASDNLAVQNLKGFSNASLGFETHGATVPIVSYLAPEKLSASTRRYE	1551	QY 1279 KOKTGIAOLVKYGLKDLPEVVGILLKGLKIGLQYGLINLGLVVKQOHOINGLIFOFVAFIKRR 1338
Db	781	TKVTDERNGRFASDNLAVQNLKGFSNASLGFETHGATVPIVSYLAPEKLSASTRRYE	840	Db 436 KOKTGIAOLVKYGLKDLPEVVGILLKGLKIGLQYGLINLGLVVKQOHOINGLIFOFVAFIKRR 495
QY	1552	TQVQTRLQTSNLHQSSSETIALLKPKETIQLQFSLWDADEQAFNTVKOLLSP	1611	QY 1339 QRAYPEIILAAAGGRYDLIIPQFRGPQALGPVPTAIGVSTADKISAAVLMNEESTVITSSCD 1398
Db	841	TQVQTRLQTSNLHQSSSETIALLKPKETIQLQFSLWDADEQAFNTVKOLLSP	900	Db 496 QRAYPEIILAAAGGRYDLIIPQFRGPQALGPVPTAIGVSTADKISAAVLMNEESTVITSSCD 555
QY	1612	KQYKLVCDIYNIKVEKVKSVFLYSTRDD	1643	QY 1399 LIVVSGMMSMRAINLTQKLWTAGTAEIMDWSQSOEELQBYCRHETTYVALVSDE
Db	901	KQYKLVCDIYNIKVEKVKSVFLYSTRDD	932	Db 616 GSHYKVKSFEKERQTERKVLTEFLDVHQLKRTKVDTAETIMDWSQSOEELQBYCRHETTYVALVSDE
RESULT	3			Db 556 LIVVSGMMSMRAINLTQKLWTAGTAEIMDWSQSOEELQBYCRHETTYVALVSDE
QH5K1	Q9H5K1	PRELIMINARY;	PRT;	QY 1459 GSHYKVKSFEKERQTERKVLTEFLDVHQLKRTKVDTAETIMDWSQSOEELQBYCRHETTYVALVSDE
ID	Q9H5K1			Db 676 QRAYPEIILAAAGGRYDLIIPQFRGPQALGPVPTAIGVSTADKISAAVLMNEESTVITSSCD
AC	Q9H5K1;			Db 676 QRAYPEIILAAAGGRYDLIIPQFRGPQALGPVPTAIGVSTADKISAAVLMNEESTVITSSCD
DT	01-MAR-2001	(TREMBLrel. 16, Created)		QY 1579 LPKETILQFLSLEWDADQAFNTVKQLSLRKPQYKLVDEIYNIKVEKVKSVFLY 1638
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		Db 736 LPKETILQFLSLEWDADQAFNTVKQLSLRKPQYKLVDEIYNIKVEKVKSVFLY 795
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		QY 1639 SYRDD 1643
DE	FLJ23358	FTS, CLONE HEP14996.		Db 796 SYRDD 800
OS	Homo sapiens (Human)			DT 01-MAY-2000 (TREMBLrel. 13, Created)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606			
RN	[1]		RESULT 4	
RP	SEQUENCE FROM N_A.	Q9U56	ID Q9U56 PRELIMINARY;	
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S.,	Q9U56;	PRT; 548 AA.	
RA	Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,	Q9U56;		
RA	Tanaka T., Nakamura Y., Isogai T., Sugano S.,	Q9U56;		

DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	OX	NCBI_TaxID=9606;
DE	PURATIVE EIF2 ALPHA KINASE (FRAGMENT).	RN	[1]
GN	GCN2.	RP	SEQUENCE FROM N.A.
OS	Homo sapiens (Human).	RC	TISSUE=TESTIS;
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RA	Duesterhoeft A., Lauber J., Meewes H.W., Gassenhuber J., Wiemann S.;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	RL	EMBL; (JAN-2000) to the EMBL/GenBank/DBJ databases.
OX	NCBI_TaxID=9606;	DR	EMBL; AL137627; CAB70849.1; -.
RN	[1]	KW	Hypothetical protein.
RP	SEQUENCE FROM N.A.	FT	NON_TER 1
RX	MEDLINE=9435990; PubMed=10504407;	SEQUENCE 191 AA;	22058 MW; B2032DAEF981C23E CRC64;
RA	Berlanga J.J., Santoyo J., de Haro C.;	Q9NSZ5	
RT	"Characterization of a mammalian homolog of the GCN2 eukaryotic initiation factor 2alpha kinase.";	Query Match	11.3%; Score 185; DB 4; Length 191;
RT	Eur. J. Biochem. 265:754-762 (1999).	Best Local Similarity	100.0%; Pred. No. 1.3e-18;
RL	EMBL; AJ243128; CAB58160.1; -.	Matches	0; Mismatches 0; Indels 0; Gaps 0;
KW	Kinase.	QY	1459 GSHYKVKSPKEKEROTEKVKLETELYDHVQLRKTIVDERGREADNLAVQNLKGFSFN 1518
FT	NON_TER 1	Db	1 GSHYKVKSPKEKEROTEKVKLETELYDHVQLRKTIVDERGREADNLAVQNLKGFSFN 60
SEQUENCE 548 AA;	62759 MW;	QY	1519 ASGLFEIIGATVYPIVSVAPEKLSASTRRYETQVQTRLQTSLANLHQKSSSTIELAVD 1578
Query Match	31.0%; Score 510; DB 4; Length 548;	Db	61 ASGLFEIIGATVYPIVSVAPEKLSASTRRYETQVQTRLQTSLANLHQKSSSTIELAVD 120
Best Local Similarity	100.0%; Pred. No. 0;	Q9QZ05	PRELIMINARY; PRT; 1648 AA.
Matches	550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC	Q9QZ05; PRELIMINARY; PRT; 1648 AA.
Db	33 LKYCIEVFRPKLDRFHKPKELCAFIDIVTSTNSFLPTAELIYTIVELIQEPALQE 1193	DT	090205; (TREMBLrel. 13, Created)
QY	1134 LKYCIEVFRPKLDRFHKPKELCAFIDIVTSTNSFLPTAELIYTIVELIQEPALQE 1193	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
Db	33 LKYCIEVFRPKLDRFHKPKELCAFIDIVTSTNSFLPTAELIYTIVELIQEPALQE 92	Db	1211 LPKETILQPSLENDADECAFNTVQKLRLQPSLEPKYCDIYNKVKVPSLFLY 180
QY	1194 RNSTYLNTNHTMLKAIILHCGTIPEDKLQSVYVILYDAVTEKLTRREVEAKFCNLSLSSNS 1253	QY	1639 SYRDD 1643
Db	93 RNSTYLNTNHTMLKAIILHCGTIPEDKLQSVYVILYDAVTEKLTRREVEAKFCNLSLSSNS 152	Db	181 SYRDD 185
QY	1254 LCLYKFTLEQKGPQLDQMLPNTINSLIKQRTGIAQLVYGLKRLQVLI 1313	RESULT	6
Db	153 LCLYKFTLEQKGPQLDQMLPNTINSLIKQRTGIAQLVYGLKRLQVLI 212	Q9QZ05	
QY	1314 NUGLIVYKVOQHNGIIFQVAFIKRQRAPELLAAGGRYDILIPQFRGPOALGPVPTAIG 1373	AC	090205; PRELIMINARY; PRT; 1648 AA.
Db	213 NUGLIVYKVOQHNGIIFQVAFIKRQRAPELLAAGGRYDILIPQFRGPOALGPVPTAIG 272	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
QY	1374 VSTAIDK1SAAVLNMEESVTISSCDLVLVSVQMSMSRAINTQKLWTAGTATEMYDWS 1433	DT	01-MAY-2001 (TREMBLrel. 16, Last annotation update)
Db	273 VSTAIDK1SAAVLNMEESVTISSCDLVLVSVQMSMSRAINTQKLWTAGTATEMYDWS 332	DE	GCN2_EIF1ALPHA_KINASE.
QY	1434 QSEELQECYCRHEITIVVALDKEGSHVKVSKFEKEROTEKVKLETELYDHVQLRKT 1493	GN	
Db	333 QSEELQECYCRHEITIVVALDKEGSHVKVSKFEKEROTEKVKLETELYDHVQLRKT 392	OS	Mus musculus (Mouse).
QY	1494 VTDERNGREADNLAVONLKGFSNSASNLVSVQMSMSRAINTQKLWTAGTATEMYDWS 1533	RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
Db	393 VTDERNGREADNLAVONLKGFSNSASNLVSVQMSMSRAINTQKLWTAGTATEMYDWS 452	RC	OX NCBI_TaxID=100900; NCBI_TaxID=9606;
QY	1554 VQTRLQTSLANLHQKSSSEIETLAVDLPKETILQFLSLDEQAFNTTVQQLSLRLPKQ 1613	RT	SEQUENCE FROM N.A.
Db	453 VQTRLQTSLANLHQKSSSEIETLAVDLPKETILQFLSLDEQAFNTTVQQLSLRLPKQ 512	RX	STRAIN=BALB/C; MEDLINE=99435390; PubMed=10504407;
QY	1614 RYKLVCDEIYNKVKVKSFLYLYSYRDD 1643	RA	"Characterization of a mammalian homolog of the GCN2 eukaryotic initiation factor 2alpha kinase.";
Db	513 RYKLVCDEIYNKVKVKSFLYLYSYRDD 542	RL	Berlanga J.J., Santoyo J., de Haro C.; RT
RESULT	5	DR	Initiation factor 2alpha kinase; R. J. de Haro C.;
Q9NSZ5	PRELIMINARY;	DR	Protein; PF00069; Pkinase; 4.
AC	PRT; 191 AA.	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
Q9NSZ5	PRELIMINARY;	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
DT	01-OCT-2000 (TREMBLrel. 15, Created)	DR	SMAP1; SM00222; SRYK; 1.
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DR	ATP-Binding; Kinase; Serine/threonine-protein kinase; Transferase.
DE	HYPOTHETICAL 22.1 KDA PROTEIN (FRAGMENT).	SEQUENCE 1648 AA;	186513 MW; F27CBBBAB31ID39B CRC64;
GN	DKP2P4 3P0612.	Q9NSZ5	Query Match 5.2%; Score 85; DB 11; Length 1648;
OS	Homo sapiens (Human).	Best Local Similarity	100.0%; Pred. No. 2.0e-78;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Matches	0; Mismatches 0; Indels 0; Gaps 0;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	QY	1395 SSCD1LVVSVQMSMSRAINTLQKLWAGITAEMDWSQSQELQEYCRHETIVVALV 1454

Db	1394	SSCDLLVVSGQMSMSRATNTQKWTAGITAEIMDQSQQEPLQETCRHHEITYVALV	1453	Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1455	SDKEGSHVVKVYKSFERQEROTERKRVLE	1419	QY 1562 LANLHQKSEETIALLDLPKETIQLQFLSLEDAEQAFNTTVKQLLSLRPLPKRYLKLVCD 1621
Db	1454	SDKEGSHVVKVYKSFERQEROTERKRVLE	1478	Db 1483 LANLHQKSEETIALLDLPKETIQLQFLSLEDAEQAFNTTVKQLLSLRPLPKRYLKLVCD 1542
RESULT	7			QY 1622 EIYNKVEKKVSVLFLYSYRDD 1643
Q9ESBB		PRELIMINARY;	PRT;	Db 1543 EIYNKVEKKVSVLFLYSYRDD 1564
ID	Q9ESBB;			
AC		PRELIMINARY;	PRT;	
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		
DE	GCN2ALPHA;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OC	NCBI_TaxID=10090;			
OX	RNA	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/C;			
RX	MEDLINE=201507056;	PubMed=10655230;		
RA	Sood R., Porter A.C., Olsen D.A., Cavener D.R., Wek R.C.;			
RT	"A mammalian homologue of GCN2 protein kinase important for translational control by phosphorylation of eukaryotic initiation factor-2alpha."			
RT	Genetics 154:787-801(2000).			
DR	EMBL; AF193342; AAG22589.1;			
SQ	SEQUENCE 1370 AA; 154054 MW;	AAFF8A7C22608681E CRC64;		
Query Match	5.0%	Score 82; DB 11; Length 1370;		
Best Local Similarity	100.0%	Pred. No. 3.1e-15;		
Matches	82;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1562 LANLHQKSEETIALLDLPKETIQLQFLSLEDAEQAFNTTVKQLLSLRPLPKRYLKLVCD 1621	Query Match 5.0%; Score 82; DB 11; Length 1648;		
Db	1283 LANLHQKSEETIALLDLPKETIQLQFLSLEDAEQAFNTTVKQLLSLRPLPKRYLKLVCD 1342	Best Local Similarity 100.0%; Pred. No. 3.6e-75;		
Qy	1622 EIYNKVEKKVSVLFLYSYRDD 1643	Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	1343 EIYNKVEKKVSVLFLYSYRDD 1364			
RESULT	8			QY 1562 LANLHQKSEETIALLDLPKETIQLQFLSLEDAEQAFNTTVKQLLSLRPLPKRYLKLVCD 1621
Q9ESB6		PRELIMINARY;	PRT;	Db 1561 LANLHQKSEETIALLDLPKETIQLQFLSLEDAEQAFNTTVKQLLSLRPLPKRYLKLVCD 1620
ID	Q9ESB6;			QY 1622 EIYNKVEKKVSVLFLYSYRDD 1643
AC		PRELIMINARY;	PRT;	Db 1621 EIYNKVEKKVSVLFLYSYRDD 1642
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DE	GCN2GAMMA.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OC	NCBI_TaxID=10090;			
OX	RNA	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/C;			
RX	MEDLINE=201507056;	PubMed=10655230;		
RA	Sood R., Porter A.C., Olsen D.A., Cavener D.R., Wek R.C.;			
RT	"A mammalian homologue of GCN2 protein kinase important for translational control by phosphorylation of eukaryotic initiation factor-2alpha."			
RT	Genetics 154:787-801(2000).			
DR	EMBL; AF193342; AAG22591.1;			
SQ	SEQUENCE 1570 AA; 177825 MW;	00E3B8D7E926D130 CRC64;		
Query Match	5.0%	Score 82; DB 11; Length 1570;		
Best Local Similarity	100.0%	Pred. No. 3.5e-5;		

AC	O9VWB2;		161	HVKIGDFGLAT 171
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DE	POLO PROTEIN.			
GN	DROSOPHILA melanogaster (Fruit fly).			
OS	Eukarya; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OX	Hydrozoa; Drosophilidae; Drosophila.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY			
RX	Medline=20196006; PubMed=10731132;			
RA	Adams M.D., Celrniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatullah P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Branden R.C., Rogers Y.-H.C., Blazquez M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.C., Heit G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietzsch S.M., Dodson K., Doupe L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Gloedek A., Gong F., Gorrell J.P., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman J.R., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitt A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishashina N.V., Mobarry C., Morris J., Moshrefi A., Mount D.R., Nelson K.A., Nixon D., Nusskern D.R., Paclob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Rennington K., Saunders R., Scheeler F., Shen H., Shue B.C., Sinden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirska R., Tector C., Turner E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT The genome sequence of <i>Drosophila melanogaster</i> ; ; RL Science 287:2185-2195(2000)	RESULT 15		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT The genome sequence of <i>Drosophila melanogaster</i> ; ;	019055	PRELIMINARY;	
RA	CC -1 SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES	019055		
DR	EMBL; AE03514; AA49036.1 - .	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
DR	InterPro; IPR002290; - .	019055		
DR	Pfam; PF00069; Pkinase; 1.	019055		
DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
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DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
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DR	InterPro; IPR002290; - .	019055		
DR	Pfam; PF00069; Pkinase; 1.	019055		
DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
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DR	Pfam; PF00069; Pkinase; 1.	019055		
DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
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DR	Pfam; PF00069; Pkinase; 1.	019055		
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DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
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Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
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DR	InterPro; IPR002290; - .	019055		
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DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
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Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
DR	InterPro; IPR002290; - .	019055		
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DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
DR	InterPro; IPR002290; - .	019055		
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DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
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DR	InterPro; IPR000719; - .	019055		
DR	InterPro; IPR002290; - .	019055		
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DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
DR	InterPro; IPR002290; - .	019055		
DR	Pfam; PF00069; Pkinase; 1.	019055		
DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
DR	InterPro; IPR002290; - .	019055		
DR	Pfam; PF00069; Pkinase; 1.	019055		
DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
DR	InterPro; IPR002290; - .	019055		
DR	Pfam; PF00069; Pkinase; 1.	019055		
DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
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DR	Pfam; PF00069; Pkinase; 1.	019055		
DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
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DR	Pfam; PF00059; POLO_box; 2.	019055		
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DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		
Query Match	0.7%	Score 11;	DB 5;	Length 576;
Best Local Similarity	100.0%	Pred. No. 0.051;		
Matches	11;	Conservative	0;	Mismatches 0;
DR	InterPro; IPR000719; - .	019055		
DR	InterPro; IPR002290; - .	019055		
DR	Pfam; PF00069; Pkinase; 1.	019055		
DR	Pfam; PF00059; POLO_box; 2.	019055		
DR	Prosite; PS50011; PROTEIN_KINASE_DOM; 1.	019055		
DR	Prosite; PS00108; PROTEIN_KINASE_ST; 1.	019055		
DR	SMART; SM00220; S_TK; 1.	019055		
KW	ATP-binding; Serine/threonine-protein kinase; Transferase.	019055		
DR	SEQUENCE 576 AA; 66973 MW; 5022BAC0E888FAD CRC64;	019055		

PROSITE PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE PS00108; PROTEIN_KINASE_ST; 1.
DR SMART; SM00220; S_TKC; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase;
KW Tyrosine-protein kinase.
FT NON_TER 1 1
SEQUENCE 301 AA; 34230 MW; 3512983ADF5D1A3B CRC64;

Query Match 0.6%; Score 10; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 862 VKIGDFGLAT 871
Db 135 VKIGDFGLAT 144

Search completed: October 22, 2001, 01:31:30
Job time: 271 sec